

100

APPENDIX APRIMERS DESIGNED FOR DEN-2 CLONING/SEQUENCING PROJECT:

SEQ. ID NO.	PRIMER	MER/SENSE	SEQUENCE
3	pUC/M13-P5	25/+	5'-CCAGTCACGACGTTGAAAAACGAC-3'
4	pUC/M13-P5B	27/+	5'-GGATGTGCTGCAAGGCCATTAAAGTTGG-3'
5	pUC/M13-P3	25/+	5'-TGAGCGGATAACAATTTCACACAGG-3'
6	pUC/M13-P3B	27/-	5'-GCCTTACACTTATGCTTCCGGCTCG-3'
7	D2-1-ECO.T7 75/+		5'-GCGGATATTG/GAATTC/TCTAGA/ AAATTAATACGACTCACTATA/ AGTTGTTAGTCTACGTGGACCGACAAAGACAG-3' (5'-Fill /EcoRI /XbaI/T7 Promoter/ 5'-end of DEN-2)
8	D2-SMT71	77/+	5'-CCAGT/GAATTC/GAGCTC/AAGCGT/ AAATTTAACACGACTCACTATA/ AGTTGTTAGTCTACGTGGACCGACAAAGACAG-3' (5'-Fill/EcoRI/SstI/MluI/T7 Promoter/ 5'-end of DEN-2)
9	D2-1	24/+	5'-AGTTGTTAGTCTACGTGGACCGAC-3'
10	D2-28	34/+	5'-GACAGATTCTTGAGGGAGCTGAGCTAACGTAG-3'
11	D2-134	28/+	5'-TCAATATGCTGAAACGGAGAGAAAACCG-3'
12	cD2-250	26/-	5'-GGGATTGTTAGGAAACGAAGGAACGC-3'
13	D2-274	32/+	5'-CCACCAAACAGCAGGGATACTGAAAAGATGGGG-3'
14	cD2-378	25/-	5'-TGCAGATCTCGTCTCTTATTCAAG-3'
15	D2-528	25/+	5'-CGTGAACATGTGTACCCCATGGCC-3'
16	cD2-616	26/-	5'-TTGCACCAACAGTCATGTCTTCAGG-3'
17	D2-616	25/+	5'-ACCAGAACATAGATTGTTGGTGC-3'
18	cD2-618	25/-	5'-GCACCAAACAGTCTATGTTCTGGC-3'
19	cD2-771	25/-	5'-ATGTTCCAGGCCCTCTGATGAC-3'
20	D2-847	25/+	5'-GCAGCAATCCTGGCATACACCATAG-3'
21	D2-996	27/+	5'-GGTTGACATAGTCTTAGAACATGGAAG-3'
22	cD2-996	27/-	5'-CTTCCATGTTCTAAGACTATGTCAACC-3'

SEQ. ID NO:	PRIMER	MER/SENSE	SEQUENCE
23	D2-1005	35/+	5'-GTCTTAGAACATGGAAGTGTGTGACGACGATGGC-3'
24	D2-1141	25/+	5'-ACAAACAGAACATCGCTGCCAACAC-3'
25	D2-1211	25/+	5'-GCAAACACTCCATGGTAGACAGAGG-3'
26	cD2-1211	25/-	5'-CCTCTGTCTACCATGGACTGTTGC-3'
27	cD2-1227	27/-	5'-CCACATCCATTCCCCATCCTCTGTCT-3'
28	D2-1261	30/+	5'-GGAAAGGGAGGCATTGTGACCTGTGCTATG-3'
29	D2-1416	28/+	5'-GGAAATCAAATAACACCAACAGAGTTCC-3'
30	cD2-1503	34/-	5'-CTGCAGCAACACCATCTCATTTGAAAGTCGAGGCC-3'
31	D2-1510	25/+	5'-GACTTCAATGAGATGGTGTGCTGCTGC-3'
32	cD2-1510	25/+	5'-GCAGCAGCACCATCTCATTAAGTC-3'
33	D2-1546	28/+	5'-AAGCTTGCTGGTGCACAGGCAATGGTT-3'
34	cD2-1567	27/-	5'-TGGTAACGGCAGGTCTAGGAACCATTG-3'
35	D2-1777	23/+	5'-GGACATCTCAAGTGCAGGCTGAG-3'
36	cD2-1777	23/+	5'-CTCAGCCTGCACTTGAGATGTCC-3'
37	D2-1863	27/+	5'-GAAGGAATAGCAGAACACAACATGG-3'
38	cD2-1888	33/-	5'-CCCTTCATATTGTACTCTGATAACTATTGTTCC-3'
39	D2-2047	32/+	5'-CCTCCATTGGAGACAGCTACATCATCATAGG-3'
40	cD2-2047	32/-	5'-CCTATGATGATGTAGCTGTCTCGAACATGGAGG-3'
41	D2-2170	29/+	5'-ATGGCCATTAGGTGACACAGCCTGGGA-3'
42	cD2-2200	27/-	5'-TGTAAACACTCCCTCCCAGGGATCCAAA-3'
43	D2-2308	29/+	5'-CTCATAGGAGTCATTATCACATGGATAGG-3'
44	cD2-2504	35/-	5'-GGGGATTCTGGTTGGAACCTTATATTGTTCTGTCC-3'
45	cD2-2622	30/-	5'-TGATTCAATTCTGGTGTATTGTTCCAC-3'
46	D2-2702	25/+	5'-AAGGAATCATGCAGGCAGGAAACG-3'
47	cD2-2864	22/-	5'-ACTTCCAGCGAGTTCCAAGCTC-3' A A
48	D2-2992	25/+	5'-AACAGAGCCGTCCATGCCATATGG-3'
49	cD2-3105	22/-	5'-TCCATTGCTCCAAAGGGTGTGT-3' G
50	D2-3236	25/+	5'-AGCTTGAGATGGACTTTGATTCTG-3'

SEQ. ID NO:	PRIMER	MER/SENSE	SEQUENCE
51	cD2-3410	22/-	5'-GGTCTGATTCCATCCCGTACC-3'
52	D2-3621	23/+	5'-GTCCTTAGAGAGACCTGGAAAGAG-3'
53	cD2-3739	25/-	5'-GTTTCTCAAGAGTAGTCCAGCTGC-3' C
54	D2-3905	25/+	5'-ATCAATTGGCAGTGACTATCATGGC-3'
55	cD2-4002	25/-	5'-TGTTAAGAGCAGTGGAGAACGGAC-3' A G
56	cD2-4060	25/-	5'-GATTGAGACCTTGTATCGTCAACGC-3'
57	D2-4214	25/+	5'-TGACAGGACCATTAGTGCTGGAGG-3'
58	D2-4257	34/+	5'-CGTGCTCACTGGACGATCGGCCGATTTGAACTG-3'
59	cD2-4323	24/-	5'-GGGCTGCTTCTGTATATTCTGCC-3' C
60	D2-4497	25/+	5'-CCTGTGGGAAGTGAAGAACAAACGG-3'
61	cD2-4557	30/-	5'-GCTCCATCTTCCAGTTCTGACCTTCCCCTG-3'
62	cD2-4615	25/-	5'-CTCCGGCTCCBCTGAGAGTATCC-3' G G A
63	D2-4746	25/+	5'-CCTAATATCATATGGAGGAGGCTGG-3'
64	D2-4792	25/+	5'-GAAGGAGAAGAAGTCCAGGTATTGG-3'
65	cD2-4922	25/-	5'-CTGTCGACAATTGGAGATCCTGACG-3' T T
66	D2-4994	25/+	5'-GTOGAGCATATGTGAGTGCTATAGC-3'
67	D2-5124	25/+	5'-TCTGACTATGGCGGGAGGTATCTC-3'
68	D2-5173	25/+	5'-ACATTAATCTGGCCCCCACTAGAG-3'
69	cD2-5272	19/-	5'-CGATCTCCCGCCCGGTGTG-3' A
70	cD2-5318	25/-	5'-CTAACTGGTGATAGCAGCCTCATGG-3'
71	cD2-5656	27/-	5'-CCTACTGAGTTGTATCACCTTCCTTCC-3'
72	cD2-5891	26/-	5'-TGGATTCTCTCTATTCTCCCTCTTC-3'
73	D2-5770	25/+	5'-TTCAAGGCTGAGAGGGTTATAGACC-3'
74	D2-6152	25/+	5'-TCTGGTTGGCCTACAGAGTGGCAGC-3'
75	cD2-6252	27/-	5'-CCTTCTTTGTCCAGATTCCACTTCC-3' A

SEQ. ID NO:	PRIMER	MER/SENSE	SEQUENCE
76	D2-6493	35/+	5'-GCGTACRACCATGCTCTCAGTGAAC TGCCGGAGAC-3'
77	cD2-6605	24/-	5'-TTCCCAGGGTCATCTTCCCTATAAC-3' G
78	cD2-6624	31/-	5'-GATUCTAGCCGTGATTATGCGGCACATCCC-3'
79	D2-6748	25/+	5'-AAACAGAGAACACCCCCAAGACAACC-3'
80	cD2-6932	21/-	5'-CGGCATACAGCGTCCATGCTG-3'
81	D2-7055	25/+	5'-GTCCTGGGAAAGGATGGCCATTGTC-3'
82	cD2-7195	25/-	5'-CTCTGGTTGCTTTGCTTAAGTCC-3' A G G
83	cD2-7217	27/-	5'-CCGCCGCTGCTCTTTCTGAGCTTCTC-3'
84	D2-7378	25/+	5'-AGGACTACATGGGCTCTGTGTGAGG-3'
85	cD2-7515	19/-	5'-GAGAAAGTCCAGCTCCGGCC-3'
86	D2-7769	25/+	5'-AGAGAAAACATGGTCACACCAGAAGG-3'
87	cD2-7885	22/-	5'-GTTCTTOGTGTCCCTGGCCTCC-3'
88	D2-8165	25/+	5'-GGAAATATGGAGGAGCCTAGTGAGG-3'
89	cD2-8210	22/-	5'-ACCCAGTACATCTCATGTGTGG-3'
90	D2-8428	28/+	5'-GAGCATGAAACATCATGGCACTATGACC-3'
91	D2-8440	25/+	5'-TCATGGCACTATGACCBAGACCACC-3'
92	cD2-8529	22/-	5'-CAGTCTGACCACTCCGTTGACC-3' C A G
93	D2-8773	25/+	5'-AAGGTGAGAAGCAATGCAGCCTTGG-3'
94	D2-8798	29/+	5'-GGGCCATATTCACTGATGAGAACAAAGTGG-3'
95	cD2-8865	22/-	5'-TCTTTCCCTGTCAACCAGCTCC-3' C T
96	D2-9046	25/+	5'-AATGAAGATCACTGGTTCTCCAGAG-3'
97	D2-9131	25/+	5'-ACGTGAGCAAGAAAGACGGAGGAGC-3'
98	cD2-9166	22/-	5'-TGTCCCATCCTGCTGTGTCACTC-3' A G
99	cD2-9234	30/-	5'-GCTAGTTCTGTGTTCTCCCTTCCATGTGG-3'
100	D2-9344	25/+	5'-TCATATCGAGAAGAGACCAAAGAGG-3'
101	cD2-9429	24/-	5'-ACTCCTTCTCCCTCCATCTGTCTG-3'

SEQ. ID NO.	PRIMER	MER/SENSE	SEQUENCE
			104
102	cD2-9438	27/-	5'-ATGCTTTGAAGA <u>A</u> TCCCTC <u>C</u> CCCTCC-3'
103	cD2-9468	32/-	5'-GCACAGGGATTCTTC <u>T</u> GATGGT <u>G</u> AGGTGC-3'
104	D2-9645	25/+	5'-ACA <u>T</u> GGGAAC <u>C</u> TC <u>A</u> AGAGGA <u>T</u> GG-3'
105	D2-9656.BAM	45/+	5'-TTATCACATT/GGATCC/TTCA <u>A</u> GG <u>G</u> ATGG <u>A</u> ATGATTGGAC <u>C</u> AA <u>G</u> -3'
			(5'-Fill/BamHI/DEN-2 Sequence)
106	cD2-9668	28/-	5'-CAGAAGGG <u>C</u> ACTTG <u>T</u> G <u>T</u> CCA <u>A</u> TC <u>T</u> CC-3'
107	cD2-9779	21/-	5'-CT <u>C</u> CG <u>T</u> GG <u>A</u> <u>A</u> TT <u>C</u> GG <u>G</u> CT <u>C</u> -3' T G
108	cD2-9796	28/-	5'-CCGT <u>C</u> CCC <u>G</u> CA <u>A</u> AG <u>A</u> CC <u>C</u> CC <u>T</u> G <u>C</u> CC-3'
109	cD2-9796.XBA	44/-	5'-TTATCACCT <u>A</u> /TCT <u>A</u> GA/CCG <u>T</u> CT <u>CCC</u> GCAA <u>A</u> GG <u>A</u> CC <u>AC</u> CC <u>T</u> G <u>C</u> CC-3'
110	cD2-9913	26/-	5'-GTT <u>G</u> GA <u>AC</u> CC <u>A</u> AT <u>T</u> G <u>A</u> GG <u>T</u> ACT <u>G</u> C-3'
111	D2-9937	25/+	5'-ACA <u>AG</u> TC <u>G</u> AA <u>C</u> AC <u>AC</u> CT <u>GG</u> CC <u>AT</u> AC <u>A</u> -3'
112	cD2-9977	21/-	5'-GCAT <u>G</u> T <u>T</u> CC <u>G</u> T <u>G</u> TC <u>AT</u> CC-3' T
113	cD2-10003	25/-	5'-CT <u>T</u> GA <u>AT</u> CC <u>AC</u> CC <u>CT</u> G <u>T</u> CC <u>AG</u> AC-3'
114	D2-10203	25/+	5'-ATACACAGATTAC <u>AT</u> GC <u>CC</u> AT <u>CC</u> AT <u>G</u> -3'
115	cD2-10261	21/-	5'-TT <u>T</u> GC <u>T</u> CT <u>C</u> TA <u>CC</u> AC <u>AG</u> AC-3' T A
116	D2-10289	25/-	5'-GAA <u>AC</u> AA <u>AG</u> GT <u>A</u> AG <u>T</u> C <u>AG</u> GT <u>CG</u> -3'
117	cD2-10337	23/-	5'-GAC <u>GG</u> GG <u>G</u> CT <u>C</u> AC <u>AG</u> GT <u>AG</u> CA <u>TA</u> AG-3'
118	D2-10418	25/+	5'-GC <u>T</u> GT <u>AG</u> CT <u>CC</u> AC <u>CT</u> G <u>AG</u> AA <u>AG</u> GT <u>G</u> -3'
119	D2-10470	25/+	5'-GGA <u>AG</u> GT <u>G</u> T <u>AC</u> G <u>C</u> AT <u>GG</u> GT <u>AG</u> GT <u>G</u> -3'
120	cD2-10530	19/-	5'-GG <u>GC</u> CC <u>CC</u> GT <u>T</u> GT <u>GG</u> GT <u>G</u> -3' A
121	cD2-10687	59/-	5'-AGAAC <u>CT</u> GT <u>G</u> ATT <u>CA</u> AC <u>AG</u> CA <u>CC</u> AT <u>CC</u> AT <u>TT</u> CT <u>G</u> -3'
122	cD2-10687.XBA	59/-	5'-TTATCACCT <u>A</u> /GC <u>AT</u> GC/T <u>C</u> T <u>A</u> GA/ AGAAC <u>CT</u> GT <u>G</u> ATT <u>CA</u> AC <u>AG</u> CA <u>CC</u> AT <u>CC</u> AT <u>TT</u> CT <u>G</u> -3'
			(5'-Fill/SphI/XbaI/ 3'-End DEN-2 Sequence)
123	cD2-10687.X2	52/-	5'-TTATCACCT <u>A</u> /T <u>C</u> T <u>A</u> GA/ GA <u>AC</u> CT <u>GT</u> GT <u>G</u> ATT <u>CA</u> AC <u>AG</u> CA <u>CC</u> AT <u>CC</u> AT <u>TT</u> CT <u>G</u> -3'
			(5'-Fill/XbaI/ 3'-End DEN-2 Sequence)